

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/226,248ADATE: 09/07/94
TIME: 12:55:20

INPUT SET: S25.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Griffeth, Irwin J.;
Pollock, Joanne;
Bond, Julian F.;
Garman, Richard D;
Kuo, Mei-Chang;
Yeung, Siu-mei H.;
Brauer, Andrew;
Exley, Mark A.;
Powers, Steven P.

ENTERED

(ii) TITLE OF INVENTION: Allergenic Proteins And Peptides From
Japanese Cedar Pollen

(iii) NUMBER OF SEQUENCES: 201

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc.
(B) STREET: 610 Lincoln St
(C) CITY: Waltham
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02154

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/226,248
(B) FILING DATE: April 8, 1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/938,990
(B) FILING DATE: September 1, 1992

(A) APPLICATION NUMBER: PCT/US93/00139
(B) FILING DATE: January 15, 1993

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47 (viii) ATTORNEY/AGENT INFORMATION:
48 (A) NAME: Darlene A. Vanstone
49 (B) REGISTRATION NUMBER: 35,729
50 (C) REFERENCE/DOCKET NUMBER: 025.5 US (IMI-028CP)
51
52 (ix) TELECOMMUNICATION INFORMATION:
53 (A) TELEPHONE: (617) 466-6000
54 (B) TELEFAX: (617) 466-6040
55
56
57 (2) INFORMATION FOR SEQ ID NO:1:
58
59 (i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 1337 base pairs
61 (B) TYPE: nucleic acid
62 (C) STRANDEDNESS: single
63 (D) TOPOLOGY: linear
64
65 (ii) MOLECULE TYPE: cDNA to mRNA
66
67 (vi) ORIGINAL SOURCE:
68 (A) ORGANISM: Crytpomeria japonica
69
70 (ix) FEATURE:
71 (A) NAME/KEY: CDS
72 (B) LOCATION: 66..1187
73
74 (ix) FEATURE:
75 (A) NAME/KEY: mat_peptide
76 (B) LOCATION: 129..1187
77
78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
79
80 AGTCAATCTG CTCATAATCA TAGCATAGCC GTATAGAAAG AAATTCTACA CTCTGCTACC 60
81
82 AAAAA ATG GAT TCC CCT TGC TTA GTA GCA TTA CTG GTT TTC TCT TTT 107
83 Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe
84 -21 -20 -15 -10
85
86 GTA ATT GGA TCT TGC TTT TCT GAT AAT CCC ATA GAC AGC TGC TGG AGA 155
87 Val Ile Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg
88 -5 1 5
89
90 GGA GAC TCA AAC TGG GCC CAA AAT AGA ATG AAG CTC GCA GAT TGT GCA 203
91 Gly Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala
92 10 15 20 25
93
94 GTG GGC TTC GGA AGC TCC ACC ATG GGA GGC AAG GGA GGA GAT CTT TAT 251
95 Val Gly Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr
96 30 35 40
97
98 ACG GTC ACG AAC TCA GAT GAC GAC CCT GTG AAT CCT GCA CCA GGA ACT 299
99 Thr Val Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly Thr

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	45	50	55	
100				
101				
102	CTG CGC TAT GGA GCA ACC CGA GAT AGG CCC CTG TGG ATA ATT TTC AGT			347
103	Leu Arg Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser			
104	60	65	70	
105				
106	GGG AAT ATG AAT ATA AAG CTC AAA ATG CCT ATG TAC ATT GCT GGG TAT			395
107	Gly Asn Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr			
108	75	80	85	
109				
110	AAG ACT TTT GAT GGC AGG GGA GCA CAA GTT TAT ATT GGC AAT GGC GGT			443
111	Lys Thr Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly			
112	90	95	100	105
113				
114	CCC TGT GTG TTT ATC AAG AGA GTT AGC AAT GTT ATC ATA CAC GGT TTG			491
115	Pro Cys Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly Leu			
116	110	115	120	
117				
118	TAT CTG TAC GGC TGT AGT ACT AGT GTT TTG GGG AAT GTT TTG ATA AAC			539
119	Tyr Leu Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn			
120	125	130	135	
121				
122	GAG AGT TTT GGG GTG GAG CCT GTT CAT CCT CAG GAT GGC GAT GCT CTT			587
123	Glu Ser Phe Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu			
124	140	145	150	
125				
126	ACT CTG CGC ACT GCT ACA AAT ATT TGG ATT GAT CAT AAT TCT TTC TCC			635
127	Thr Leu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser			
128	155	160	165	
129				
130	AAT TCT TCT GAT GGT CTG GTC GAT GTC ACT CTT ACT TCG ACT GGA GTT			683
131	Asn Ser Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val			
132	170	175	180	185
133				
134	ACT ATT TCA AAC AAT CTT TTT TTC AAC CAT CAT AAA GTG ATG TTG TTA			731
135	Thr Ile Ser Asn Asn Leu Phe Phe Asn His His Lys Val Met Leu Leu			
136	190	195	200	
137				
138	GGG CAT GAT GAT GCA TAT AGT GAT GAC AAA TCC ATG AAG GTG ACA GTG			779
139	Gly His Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val			
140	205	210	215	
141				
142	GCG TTC AAT CAA TTT GGA CCT AAC TGT GGA CAA AGA ATG CCC AGG GCA			827
143	Ala Phe Asn Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala			
144	220	225	230	
145				
146	CGA TAT GGA CTT GTA CAT GTT GCA AAC AAT AAT TAT GAC CCA TGG ACT			875
147	Arg Tyr Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro Trp Thr			
148	235	240	245	
149				
150	ATA TAT GCA ATT GGT GGG AGT TCA AAT CCA ACC ATT CTA AGT GAA GGG			923
151	Ile Tyr Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly			
152	250	255	260	265

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153
154 AAT AGT TTC ACT GCA CCA AAT GAG AGC TAC AAG AAG CAA GTA ACC ATA      971
155 Asn Ser Phe Thr Ala Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr Ile
156                270                275                280
157
158 CGT ATT GGA TGC AAA ACA TCA TCA TCT TGT TCA AAT TGG GTG TGG CAA      1019
159 Arg Ile Gly Cys Lys Thr Ser Ser Ser Cys Ser Asn Trp Val Trp Gln
160                285                290                295
161
162
163 TCT ACA CAA GAT GTT TTT TAT AAT GGA GCT TAT TTT GTA TCA TCA GGG      1067
164 Ser Thr Gln Asp Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly
165                300                305                310
166
167 AAA TAT GAA GGG GGT AAT ATA TAC ACA AAG AAA GAA GCT TTC AAT GTT      1115
168 Lys Tyr Glu Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val
169                315                320                325
170
171 GAG AAT GGG AAT GCA ACT CCT CAA TTG ACA AAA AAT GCT GGG GTT TTA      1163
172 Glu Asn Gly Asn Ala Thr Pro Gln Leu Thr Lys Asn Ala Gly Val Leu
173                330                335                340                345
174
175 ACA TGC TCT CTC TCT AAA CGT TGT TGATGATGCA TATATTCTAG CATGTTGTAC      1217
176 Thr Cys Ser Leu Ser Lys Arg Cys
177                350
178
179 TATCTAAATT AACATCAACA AGAAAAATATA TCATGATGTA TATTGTTGTA TTGATGTCAA      1277
180
181 AATAAAAAATG TATCTTTTAC TATTAAAAAA AAAAAATGATC GATCGGACGG TACCTCTAGA      1337
182
183 (2) INFORMATION FOR SEQ ID NO:2:
184
185     (i) SEQUENCE CHARACTERISTICS:
186         (A) LENGTH: 374 amino acids
187         (B) TYPE: amino acid
188         (D) TOPOLOGY: linear
189
190     (ii) MOLECULE TYPE: protein
191
192     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
193
194 Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe Val Ile
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196
197 Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg Gly Asp
198 -5                1                5                10
199
200 Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala Val Gly
201                15                20                25
202
203 Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr Thr Val
204                30                35                40
205

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206 Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly Thr Leu Arg
207      45                      50                      55
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209 Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser Gly Asn
210      60                      65                      70                      75
211
212 Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr Lys Thr
213                      80                      85                      90
214
215 Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly Pro Cys
216                      95                      100                      105
217
218 Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly Leu Tyr Leu
219                      110                      115                      120
220
221 Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn Glu Ser
222      125                      130                      135
223
224 Phe Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu Thr Leu
225      140                      145                      150                      155
226
227 Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser Asn Ser
228                      160                      165                      170
229
230 Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val Thr Ile
231                      175                      180                      185
232
233 Ser Asn Asn Leu Phe Phe Asn His His Lys Val Met Leu Leu Gly His
234                      190                      195                      200
235
236 Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val Ala Phe
237      205                      210                      215
238
239
240 Asn Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala Arg Tyr
241      220                      225                      230                      235
242
243 Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro Trp Thr Ile Tyr
244                      240                      245                      250
245
246 Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly Asn Ser
247                      255                      260                      265
248
249 Phe Thr Ala Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr Ile Arg Ile
250                      270                      275                      280
251
252 Gly Cys Lys Thr Ser Ser Ser Cys Ser Asn Trp Val Trp Gln Ser Thr
253      285                      290                      295
254
255 Gln Asp Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr
256      300                      305                      310                      315
257
258 Glu Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val Glu Asn

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SEQUENCE VERIFICATION REPORT
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